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Sequence:
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd
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/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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12 US-10-359-460-22
12 US-10-098-732A-18
12 US-10-098-732A-65
3 US-99-287-849-2
12 US-10-359-460-2
12 US-10-098-732A-16
12 US-10-098-732A-16
12 US-10-098-732A-16
12 US-10-193-002-106
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US-09-287-849-26
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US-10-193-002-102
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Sequence 107, App
Sequence 12, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 21, Appl
Sequence 15, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 21, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 111, App
Sequence 111, App
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ALIGNMENTS

Sequence 107, Application US/10084843
publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355
CCRRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.

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US-10-193-002-102; Sequence 102, Applicat; Publication No. US2003; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 210121.411C9 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 107:
                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                      APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                             TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS TUBERCULOSIS
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TYPE: amino acid
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                                  COUNTRY: USA
ZIP: 98104-7092
                                                              STATE: Washington
                                                                                 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                      Application US/10193002
o. US20030135026A1
                                                                                                                                                                                       Houghton, Raymond
Vedvick, Thomas S.
Vedvick, Daniel R.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
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Dillon, Davin C.
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Pred. No. 7.1e-146;
; Mismatches 0;
                                                                                                 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
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; SEQUENCE DESCRIPTION: SEQ ID NO: 102: US-10-193-002-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                       241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                      181 LIEQAAAVEEASDTAAANQIMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                              121 LIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                      61 SSAGLMVAAASDYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                                                                                                                                                 61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                            LIATNILIGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATATLLPFEEAPEMTSAGG
                                                                                LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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Pred. No. 7.
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          300
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TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: And Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR TILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/023,040
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
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PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 391; Conserv
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Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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Campos-Neto, Antonio
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PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/253,040
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 26
LENGTH: 596
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LENGTH: 596
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Compos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Prottens of Myo
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
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ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
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                        GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                  LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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; Pred. No. 1.2e-145;
0; Mismatches 0;
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LAGANT: Brannon, Mark

APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION SAME US/10/098,732A
CURRING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 596
TYPE: PRT
ORGANTC"
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                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion ; OTHER INFORMATION: protein TbH9-Ra35 (designated MTB59F) US-10-098-732A-20
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ORGANISM: Artificial
                                                Local Similar., hes 391; Conservative
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Similarity 100.0%;
91; Conservative 0;
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MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Pred. No. 1.2e-145;
; Mismatches 0;
                                                          Score 1949; DB 12;
Pred. No. 1.2e-145;
Mismatches 0;
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                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANIOM: Artificial Sequence
; FEATURE;
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-22
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US-09-287-849-22
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PRIOR PILLING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR PILLING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILLING DATE: 1998-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/09287849 Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver.
SEQ ID NO 22
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                                                                                                                                                  Matches
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APPLICANT:
APPLICANT:
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
CURRENT FILING DATE: 1999-04-07
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                      LENGTH: 600
                                                                                                                                                                  Local Similarity 100.0%;
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 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                        MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                  Score 1949; DB 9;
Pred. No. 1.2e-145;
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TITLE OF INVENTION: Fusion protiens of Mycobacterium tuberculosis Antigens;
TITLE OF INVENTION: And Their Uses;
FILE REFERENCE: 014058-009020US;
CURRENT APPLICATION NUMBER: US/10/359,460;
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/9/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
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US-10-359-460-22
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/10359460 Publication No. US20030147911A1
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APPLICANT: Skeik
APPLICANT: Dillo
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
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                                                                                   SSAGLMVAAASPYVAWMSVTÄGQAELTÄAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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         LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 180
                                                  $$AGLMVAAA$PYVAWM$VTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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Corixa Corporation
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Skeiky, Yasir A.W.
Dillon, Davin C.
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Pred. No. 1.2e-145;
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APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 729
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local
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OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: (Ra12-TbH9-Ra35MutSA)
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APPLICANT: Guderian, Jeffrey
APPLICANT: Coriva Corporation
FITTLE OF INVENTION: Heterologous Fusion Prote
FITTLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
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US-10-098-732A-65
RESULT 11
US-09-287-849-2
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APPLICANT: Brannon,
APPLICANT: Guderian
APPLICANT: Corixa (
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Best Local (
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Pred. No. 2.2e-145;
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Application US/09287849

RESULT 12 US-10-359-460-2

Sequence 2, Application US/10359460 Publication No. US20030147911A1 GENERAL INFORMATION:

APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C.

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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Pusion Protiens of Myco
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
FULERNIT APPLICATION NUMBER: US(09/287,849)
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,556
PRIOR APPLICATION NUMBER: US 09/056,556
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ORGANISM: Artificial
FEATURE:
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Pred. No. 3.9e-145;
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; Sequence 16, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION;
; APPLICANT: Skeiky, Yasir
; APPLICANT: Brannon, Mark
; APPLICANT: Guderian, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Heterologous Fusion Pr
                                                                                                                                                                            RESULT 13
US-10-098-732A-16
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PRIOR FILING DATE: 1999-04-07
PRIOR PELICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-10-01
PRIOR PILING DATE: 1997-10-01
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 729
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
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99.7%;
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Pred. No. 3.9e-145;
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Mismatches
      Protein Constructs Comprising
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FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 16
LENGTH: 729
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of
OTHER INFORMATION: protein MTB72F
OTHER INFORMATION: fusion)
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             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
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STREET: 6300 Columbia Center,
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                                                                              OF INVENTION:
                                               OF SEQUENCES:
                                                                                                                                                                                                                                                                              Application US/10084843
                                                             Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND M
AND DIAGNOSIS C
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                                                                                                                                          Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                           Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
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Pred. No. 3.9e-145;
0; Mismatches 1;
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                                                                METHODS FOR IMMUNOTHERAPY
OF TUBERCULOSIS
701 Fifth Avenue
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                                                                                                                                                                        RESULT 15
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                                                                                               Sequence 106, Applicat Publication No. US2003 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mari Torrid T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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FILING DATE: 25-Feb-2002
CLASSIFICATION: UNKNOWND
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                       GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 391
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                    GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG
                                                                                                                                                                                                                                                                                                                                                  GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                 Application US/10193002
5. US20030135026A1
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                  Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
                                                                          Reed, Steven G.
Houghton, Raymond
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19; Mismatches
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APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
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                                    GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                         GSSGLGGGVAANLGRAASVGSLSVPQAWAAAANQAVTPAARALPLTSLTSAAERGPGQMLG
                                                                                                                                                     IVSMLNNHVSMTNSGVSMASTLHSMLKGFAP-AAAQAVETAAQNGVQAMSSLGSQLGSSL
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STATE: Washington
  GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG
                                                                            GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092
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Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Romald M.
DF INVENTION: COMPOUNDS AND M.
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84.9%; Pred. No. 1.9e-122;
tive 19; Mismatches 34; Ir
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Search completed: November 21, 2003, 17:11:03 $\,$ Job time : 34 $\,$ secs

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Result
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Perfect score:
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Listing first 45 summaries
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        and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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US-10-369-983-2
US-09-886-349A-18
US-10-369-983-21
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US-10-369-983-15
US-10-369-983-13
US-10-369-983-12
US-10-369-983-12
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US-09-886-349A-31
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US-10-384-575-51
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PCT-US02-09663A-52
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ALIGNMENTS

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APPLICANT: Reed, Steven
APPLICANT: APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: CATLAX COOPDATATION
FILE OF INVENTION: Fusion Proteins of Mycobacterium Tub
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 391
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
OTHER INFORMATION: MTB39 (TbH9FL)
US-09-886-349A-14
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US-09-886-349A-14
Sequence 14, Application US/09886349A
GENERAL INFORMATION:
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Best Local Similarity
                                       241
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                         MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                   LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                        LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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Pred. No. 8.2e-109;
O; Mismatches 0;
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APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: COTIXA Corporation
FITTLE OF INVENTION: Fusion Proteins of Mycobacterium Tub
FILE REFERENCE: 014058-009970US
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION UNMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 596
TYPE: PRT
COCANTSM: Artificial Sequence
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Sequence 2, Application US/10369983
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Pred. No. 1.3e-108;
; Mismatches 0;
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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 723
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                                                      Sequence 18, Application US/09886349A
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
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PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 60/265,737
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TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2001-02-01 NUMBER OF SEQ ID NOS: 50 SOFTWARE: PatentIn Ver. 2.1

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Sequence 21, Application US/10369983

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Skeiky, Yasir

APPLICANT: Reed, Steven

APPLICANT: Reed, Steven

APPLICANT: Corixa Corporation

FILE OF INVENTION: Fusion Proteins of Mycobacterium Tub

FILE REFERENCE: 014058-009081US

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2003-02-18

PRIOR APPLICATION NUMBER: US 60/357,351

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 21

LENGTH: 729
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; FEATURE:
; OTHER INFORMATION: Des
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Best Local Similarity
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                                                                                     Query Match
                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MTB72F
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TYPE: PRT
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ENGTH: 729
                                                                       Local Similarity
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               MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 201
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                                                          Conservative
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                                                        Score 1949; DB 6;
Pred. No. 1.6e-108;
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Pred. No. 1.6e-108;
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RESULT 6
US-10-369-983-22
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TITLE OF INVENTION: Fusion Proteins of Mycobacterium
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/10369983 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
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OTHER INFORMATION:
OTHER INFORMATION:
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TYPE: PRT
ORGANISM: Artificial Sequence
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                         LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                              LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
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LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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Pred. No. 1.6e-108;
); Mismatches 0;
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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG

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RESULT 8
US-10-369-983-14
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; GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-09081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
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APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporat
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TYPE: PRT
ORGANISM: Artificial Sequence
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                               US/10369983
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Pred. No. 1.9e-108;
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PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14
                                             SOFTWARE: PatentIn
SEQ ID NO 13
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Best Local Similarity
                                                                              APPLICANT: Skeiky, yasir
APPLICANT: Guderian, Jeff
APPLICANT: Gede, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
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APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
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TYPE: PR
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APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION UMMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
INUMBER OF 520 ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SECTUM 12
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ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
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CURRENT FILING DATE: 2003-02-18
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                                                                                   LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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Pred. No. 2.4e-108;
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PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PACENTIN Ver. 2.1
SEQ ID NO 18
LENGTH: 1016
TYPE: PRI
PRIORE: Artificial Sequence
                                  RESULT 13
US-10-369-983-17
; Sequence 17, Application US/10369983
; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
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APPLICANT: Skeiky, Yasir APPLICANT: Guderian, Jeff
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CURRENT FILING DATE: 2003-02-18
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TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence:fusion OTHER INFORMATION: MTB103F (MTB72F-85b)
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Pred. No. 2.4e-108;
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 170
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Best Local Similarity
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ORGANISM: Artificial Sequence
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                    LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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Pred. No. 2.4e-108;
; Mismatches 0;
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RESULT 14
US-10-369-983-16
; Sequence 16; Application US/10369983
; Sequence 16; Application US/10369983
; GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Courie, Jeff
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PRIOR DATE: 2002-02-15
SUMMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 1154
TYPE: PRT
CORGANISM: Artificial Sequence
FEATURE:
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FILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/99/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-02-01
PRIOR FILING DATE: 2010-02-01
PRIOR FILING DATE: 2010-02-01
SOFTWARE: PATENTIAL OF SO
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LENGTH: 729
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                                                                               Query Match
Best Local S
Matches 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09886349A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1949; DB 6; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 391; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixá Corporation
                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39 OTHER INFORMATION: fusion)
                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                        1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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                                                                               Conservative
                                                                                               99.7%;
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                                                                           Score 1944; DB 5;
Pred. No. 3.3e-108;
0; Mismatches 1;
                                                                                                               Length 729;
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202 ŚŚŚĠLMVÄÄÄŚPÝVÄWŃŚVŤÁGĄŘĽŤÄÄĠŮŘVĀÄÄÁŠĖŤÄYĠĿŤVPĖPŸĽÄĖNÄÄĖLÄI 261 121 LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLILPFEEAPEMTSAGG 180 262 LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLILPFEEAPEMTSAGG 180 262 LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLILPFEEAPEMTSAGG 321 181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLIGGLMKTVSPHRSPISN 240 241 MUSMANNHMSMTNSGVSMTNYLISSMLKGFAPAAAAQAVTAAQNGYRAMSSLGSSIGSSG 300 241 MUSMANNHMSMTNSGVSMTNYLISSMLKGFAPAAAAQAVQTAAQNGYRAMSSLGSSIGSSG 300 241 MUSMANNHMSMTNSGVSMTNYLISSMLKGFAPAAAAQAVQTAAQNGYRAMSSLGSSIGSSG 300 241 MUSMANNHMSMTNSGVSMTNYLISSMLKGFAPAAARAQAVTAAQNGVRAMSSLGSSIGSSIGSSG 300 242 LIGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360 361 GGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 501 361 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391 361 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532	dg .	Ş	ф	δδ	Db	8	Db	γQ	DЬ	γQ	Ъ	Qy
WAQDAAAMFGYAAAAXBTAXGLTVPPPVIAE		361 GQMGARAGGGLSGVLRVPPRPYVM		301 LGGGVAANLGRAASVGSLSVPQAP								61 SSAGLMVAAASPYVAWMSVTAGOA
NRĀELMI 261	 PHSPAAG 532	MPHSPAAG 391	WAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 501	WAAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360	SMLKGFAPAARQAVQTAAQNGVRAMSSLGSSG 441	SMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300	VPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381	VPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240	MWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 321	WWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 180		SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120

Search completed: November 21, 2003, 17:10:17
Job time : 21 secs

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5.1.6

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 2000000000
                                                                                                                           A Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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Copyright (c) 1993 - 2003
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Result No.	Score	* Query Match Length DB	ength		ID	Description
1	1949	100.0	391	18	AAW32449	Mycobacterium tube
N	1949	100.0	391	18	AAW32381	Mycobacterium tube
w	1949	100.0	391	19	AAW81702	M. tuberculosis im
4	1949	100.0	391	19	AAW64335	Mycobacterium tube
ហ	1949	100.0	391	20	AAY39132	. M. tuberculosis an
0	1949	100.0	391	20	AAY38989	M. tuberculosis re
7	1949	100.0	391	20	AAY04778	Mycobacterium spec
8	1949	100.0	391	22	AAU01888	M. tuberculosis an
9	1949	100.0	391	23	AAE29707	Mycobacterium sp.

	AAY:	20	263 263	60.9	1187	446
M. tuberculosi Mycobacterium	AAW81680 AAW64317	19	263 263	60.9	1187	4 2
Mycobacterium	AAW3237	18	263	•	1187	41
Mycobacterium	AAW3244	18	263	•		0
Antigenic	AAU7459	23	358		_	9
Mycobacterium	AAW3238	14	341	•	٠.	8
Mycobacterium	AAW32	18	341		٠.	7
.≾		20	359	•	۸.	6
M. tuberculosi	AAY39	21	359		٠.	ω i
	AAW6433	ب <u>بر</u> ا و	350	76.3	1486.5	4
	AAY38991		9 6		•	3 1
	AAY3913	20	396	84.8	•	Ξ
	AAW64	19	396	•	~	õ
		19	396	•	•	9
	AAU7458	23	726	97.6	10	ω
		20	729	•	1931	7
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		20	394	99.7	1944	
		22	788		1945	
		23	930	•	1949	
		22	815	•	1949	_
		22	744	•	1949	_
		23	729	•	1949	_
	AAE29709	23	729	100.0	1949	œ
		22	729	•	1949	7
	AAU7459	23	600	•	1949	σ
	AAY3206	20	600	•	1949	G
	AAU745	23	599	•	1949	4.
	AAE17	23	596	•	1949	ယ
	AAE2971	23	596	100.0	1949	N
	AAY3207	20	596	•	1949	μ
	AAE17571	23	391	100.0	1949	0

ALIGNMENTS

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RESULT 1
AAW32449
ID AAW3
XX AW3
AC AAW3
XX Myco
XX II-M
XX Myco
XX My
                                                                                                                                                                                                                        12-JUL-1996;
01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW32449;
                                   Campos-neto A, Dillon DC,
Twardzik DR, Vedvick TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9709428-A2
                                                                                                                                                     (CORI-) CORIXA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis.
                                                                                                                                                                                                                        96US-0680574.
95US-0523436.
95US-0533634.
96US-0620874.
96US-0659683.
                                                                                                                                                         CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US14674
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                                                                          Houghton R,
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                                                                              Reed
                                                                              SG,
                                                                              Skeiky YAW;
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1997-192903/17

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RRESULT 2
AAW323M
XX AAW3
XX AAW3
XX AAW3
XX BY MYCO
XX MYCO
XX Anti
XX Skin
XX WyCO
XX WyCO
XX WYCO
XX MYCO
X
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                                                                                                                                         Mycobacterium
                                                                                                                                                                                             Antigen; immunogen; vaccine; skin testing; M.tuberculosis
                                                                                                                                                                                                                                                                                  Mycobacterium
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useful in vaccines
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                                                                                                                                           tuberculosis
                                                                                                                                                                                                                                                                                  tuberculosis antigen TbH-9FL
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Pred. No. 4.8
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ion or treatment of tuberculosis, a
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01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen, TbH-9FL The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragment of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
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N-PSDB; AAT91455.
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Twardzik DR, Vedvick TH;
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                 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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96US-0620280.
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Pred. No. 4.8e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - us to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
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11-OCT-1996;
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96US-0730510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1949; DB 19;
Pred. No. 4.8e-143;
                                                                           /PQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lodes MJ;
391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises Mycobacterium tuberculosis antigen
ThH-9FL. It is encoded by genomic DNA (see AAV4435) isolated from a
M. tuberculosis strain H37RV genomic library using a probe from
C clone TbH-9 (see AAV44371). The invention relates to compositions
and methods for diagnosing tuberculosis. It provides polypeptides
(see AAW64291-W64379) comprising an antigenic portion of a soluble
M. tuberculosis antigen, as well as DNA sequences encoding such
tuberculosis antigen, as well as DNA sequences encoding such
polypeptides, recombinant expression vectors and transformed or
transfected host cells. Also claimed are methods and diagnostic
kits for detecting M. tuberculosis infection in a patient using
these polypeptides, antibodies or oligonucleotide probes and
c primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                    Matches 391;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Mycobacterium tuberculosis polypeptides and DNA - use to develop products for the detection of M. tuberculosis infection {\sf C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-251292/22
N-PSDB; AAV44395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A, D
Reed SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 133-135; 250pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis of tuberculosis
                   181
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                      LIATULLGQUTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                     LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGG 180
                                                                                                                                                                                                                SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                     MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 AA;
                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon
cy YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0818111.
96US-0729622.
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Twardzik DR, Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                    ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1949; DB 19;
Pred. No. 4.8e-143;
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿
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                                                      Matches
                                                                 Query Match
Best Local :
                                                                                                                             The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAY39083 to AAY39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis antigen TbH-9FL
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                              Example 3;
                                                                                                                                                                                                                                                                                                                                      New antigens
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                 Campos-Neto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapy; diagnosis; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis; M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY39132 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORIXA
                MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                            Page 123-124; 299pp; English.
                                                                                                                                                                                                                                                                                                                          and
                                                                                                        391
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                                                      Conservative
                                                                                                                                                                                                                                                                                                                     from Mycobacterium tuberculosis useful in diagnostic id protective or therapeutic vaccines or compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis.
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98US-0025197
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SG, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunisation;
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YAW, Twardzik DR,
                                                               Score 1949;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis; antigen; immun
nisation; vaccine; infection;
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                                                    Mismatches
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                                            DB 20; .
4.8e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                      Houghton R;
                                                    Indels
                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogen;
                                                                             391;
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                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 Antigen; vaccine;
                       This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
Sequence
                                                                                                                                            New polypeptide comprising antigenic portions
                                                                                                                                                                                WPI; 1999-527416/44.
                                                                                                                                                                                                        Campos-Neto A,
Lodes MJ, Reed
                                                                                                                                                                                                                                                                  05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                            26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis recombinant antigen protein TbH-9FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                  immunity.
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98US-0024753
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                                                                                                                       168-169;
                                                                                                                                                                                                      Dillon DC,
SG, Skeiky
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                                                                                                                                                                                                                                                                                                                                                                                                        detection; infection; antibody; immunisation;
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YAW, Twardzik DR,
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Query Match

100.0%;

Score 1949;

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20;

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RESULT 7
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                                                                                                                                 Gicquel B,
Guigueno A;
Sequences AAY04742-Y05000 and AAY07201-Y07204 represent sec-
proteins from various Mycobacterium species microorganisms.
encoding nucleotide sequences can be used as primers and pr
                                                          Mycobacterial DNA vectors containing reporter constructs identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                     WPI; 1999-181045/15.
N-PSDB; AAX34030.
                                                                                                                                                                                  11-SEP-1997;
14-AUG-1997;
                                                                                                                                                                                                                                                                                               Secreted protein; Mycobacterium; primer; PCR; hybridisation; detection; vaccine; immunisation
                                                                                                                                                                                                                                                                                                                            Mycobacterium species protein sequence
                                                                                                                                                                                                                                                                                                                                                  06-JUL-1999
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                                          Claim
                                                                                                                                                                                                                 14-AUG-1998;
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                                                                                                                                                                                                                                                                            Mycobacterium
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97FR-0010404
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ARESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. tuberculosis
                   Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens
                                                                                                    WPI; 2001-290576/30.
N-PSDB; AAS03779.
                                                                                                                                                                                     Skeiky Y,
                                                                                                                                                                                                                                                                                            07-OCT-1999;
07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
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99US-0158425
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Pred. No. 4.8e-143;
); Mismatches 0;
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RESULT 9
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents Mycobacterium tuberculosis TbH9 (also known as Mtb39A), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease. ATDS
                Skeiky
                                                                                                                                                                                                              Vaccine; immunity;
                                                                                                                                                                                                                                                                       27-JAN-2003
                                                                                                                                                                                                                                                                                                                            AAE29707 standard; Protein; 391
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                                                                     13-MAR-2001; 2001US-275837P
                                                                                               13-MAR-2002; 2002WO-US08223
                                                                                                                             19-SEP-2002.
                                                                                                                                                       WO200272792-A2
                                                                                                                                                                                                                                        Mycobacterium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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              Σ,
                                                                                                                                                                                                              diagnostic agent; gene therapy; TbH9FL antigen.
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Pred. No. 4.8e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium sp. TbH9FL antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protec immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 86-87; 155pp; English
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                                                                                                                                                 121 LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATATLLPFEEAPEMTSAGG
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                                                                  LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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        MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                        LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLLPFEEAPEMTSAGG
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                                              LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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ilarity 100.0%;
Conservative 0
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Pred. No. 4.8e-143;
; Mismatches 0;
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RESULT 10
AABI7571
ID AABI7571 standard; Protein; 391 AA.

XX
AC AABI7571;
XX
DT 22-APR-2002 (first entry)
XX
DE Mycobacterium species MTB39 (TbH9) protein #2.

XX
Eusion protein; antigen; serological sensitivity; immune response;
XX
XX
XX
CS Mycobacterium sp.
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5 B 5

GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391

391

LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV

360

LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV

MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The present invention relates to fusion proteins containing at least CC two Mycobacterium species antigens, nucleotides encoding them and CC compositions comprising such fusion proteins. The present invention CC particularly relates to nucleic acids encoding fusion proteins that CC include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with CC tuberculosis and methods for their use in diagnosis, prevention and CC treatment of tuberculosis infection. Sequences of the invention are CC useful for eliciting an immune response in a mammal, e.g., human, CC immunised with BCG. They are useful in the diagnosis, treatment and CC prevention of Mycobacterium infection. The fusion proteins and the CC polynucleotides are useful as diagnostic tools in patients infected CC with Mycobacterium, in vitro and in vivo assays for detecting humoral CC antibodies or cell-mediated immunity against M. tuberculosis, for the CC diagnosis of an infection or monitoring of disease progression, as CC patient and for raising anti-M. tuberculosis antibodies in a non-human CC animal. Sequences of the invention are useful as in vivo diagnostic agents CC fusion proteins of the invention are useful as in vivo diagnostic agents CC for intradermal skin test. The present sequence is Mycobacterium species
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising MTB39 antigen and MTB32A antigen Mycobacterium species, useful for eliciting immune respo
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01-FEB-2001; 2001US-265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 83; Page 102-103; 136pp; English.
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                                                                                    MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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MVDFGALPPBINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 199
N-PSDB;
                                                                                                                                                                                    This sequence represents a recombinant Mycobacterium tuberculosis bi-antigen fusion protein, termed Mtb59f, composed of the antigens TbH9 and Ra35. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AAZ20205) comprising the coding sequences for the 2 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW, Alderson
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30-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis antigen fusion protein Mtb59f.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 12A-B; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
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DB; AAZZ0205.
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RESULT 12
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                            The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2001; 2001US-275837P
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                                                                                                                                                                                                                                                                            Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                 New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protecimmunity against pathogenic microorganisms e.g. Leishmania and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2002;
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Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microorganisms such as Leishmania and Mycobacterium tuberculosis. Fu polypeptides are used for enhancing the expression of polymucleotide as in vivo diagnostic agents and for raising antibodies in a non-hum animal. The invention is used in gene therapy. The present sequence MTB59F fusion protein. This fusion protein comprises Ra35 protein fr Mycobacterium tuberculosis and TbH9 protein from Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                           LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                    MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1949; DB 23;
Pred. No. 8.1e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
399
                             391
                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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resent sequence is
Ra35 protein from
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RESULT 13
AAE17574
ID 17AE17
XX AAE17
AC AAE17
XX Pusic
XX Fusic
XX Fusic
XX Fusic
XX Wycob
XX Wycob
XX Wycob
XX Wycob
XX Wo200
XX W0200
X
                                              N-PSDB; AAD28344
                                                                                    WPI; 2002-147798/19
                                                                                                                                                                Skeiky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2001; 2001WO-US19959
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infection;
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                                                                                                                                                                                                                                                 CORP
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two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention comparising such fusion proteins. The present invention comparising such fusion proteins. The present invention comparisions comprising such fusion proteins. The present invention comparision controlled to the protein of the protein colors and sensitivity of sera from individuals infected with controlled to tuberculosis and methods for their use in diagnosis, prevention and controlled to the colors of the invention and in vivo assays for detecting humoral controlled to generate or cell-mediated immunity against M. tuberculosis, for the colors of an infection or monitoring of disease progression, as compared to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human colors of the invention are also used as vaccines. MTB32A controlled the colors of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species.
RESULT 14
AAU74599
ID AAU74
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AC AAU74
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DT 08-MA
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DE Antig
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Best Local S
Matches 391
                                                         08-MAY-2002
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                 Antigenic
                                                                                                                                  AAU74599
                                                                                                                                                                                                                                                                                                                                                                                                                                                           189
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                                                                                                                                standard;
                                                                                                                                                                                                                                                GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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                                                                                                                                                                                                                            GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                                                                                                     LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                         LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
               fusion protein Tb59-Ra35
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                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                Protein;
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Pred. No. 8.1e-143;
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                   (Mtb59f).
                                                                                                                                                                                                                                                                391
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Matches 391
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07-APR-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                       The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention ar useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed
                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins of Mycobacterium tuberculosis antigens, useful for diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein; tuberculosis; Mycobacterium tuberculosis; tuberculostatic; immunogen; vaccine; Tb59-Ra35; Mtb59f.
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                  as an immunogen to tuberculosis. This
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 12; 62pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-1999;
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                                                                                                                                                                                                          Local Similarity
 189
                         181
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                                                                                                                                                                                                                                                                       invention.
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK14139
                                                               LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                              MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
               LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                599
                                                                                                                                                                                                Conservative
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97US-0942578.
98US-0025197.
98US-0056556.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "OTHER= Xaa. Xaa=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= OTHER
                                                                                                                                                                                                                                                                                  induce and/or enhance an immune response to M. sequence represents an M. tuberculosis fusion
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                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                          Score 1949; DB 23;
Pred. No. 8.1e-143;
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241

MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG

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RESULT 15
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                                                                                                                                                                         Query Match
Best Local Sim:
Matches 391;
                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a recombinant Mycobacterium tuberculosis tri-antigen fusion protein, termed Mtb61f, composed of the antigens TbH9, DPV and MTI. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AAZ20203) comprising the coding sequences for the 3 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
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30-DEC-1998;
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                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 10A-B; 83pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-601610/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen fusion protein Mtb61f.
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                     GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                              MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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Search completed: November 21, 2003, 17:04:07 Job time : 46 secs

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Listing first 45 summaries
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US-08-818-111-106
US-09-072-596-104
US-09-072-596-104
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US-09-073-09-122
US-09-073-009-122
US-09-073-009-123
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US-08-311-731A-208
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Sequence 102, App
Sequence 104, App
Sequence 21, Appli
Sequence 116, App
Sequence 116, App
Sequence 110, App
Sequence 109, App
Sequence 104, App
Sequence 104, App
Sequence 91, Appl
Sequence 92, Appl
Sequence 92, Appl
Sequence 126, App
Sequence 127, Appl
Sequence 128, Appl
Sequence 131, App
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ALIGNMENTS

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RESULT 1
US-08-818-112-107
; Sequence 107, Application US/08818112
                                                                              US-08-818-112-107
                                                                                                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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GENERAL INFORMATION:
                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                     Query Match
    Matches
                  Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington COUNTRY: USA
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    391;
    Conservative
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                    100.0%; Score 1949; DB 3; 100.0%; Pred. No. 2.7e-154;
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 US-08-818-111-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/818,111
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                         ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A
                                                                                                       REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622,4900
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          STREET:
                         STRANDEDNESS:
                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
               TOPOLOGY:
                                                   LENGTH:
                                                                                                                                                                NAME: Maki,
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Vedvick, Thomas S.
Twardzik, Daniel R.
VENTION: COMPOUNDS AND METHODS
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Dillon, Davin C.
Campos-Neto, Antonia
                                                   391 amino acids
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STRANDEDNESS:
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Sequence 107, Application US/09056556 Patent No. 6350456
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Best Local Similarity 100.
Matches 391; Conservative
                                                                                                                                                                                                ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, \

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998

CLASSIFICATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS A
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                           TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 C
CITY: Seattle
STATE: Washing
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ZIP: 98104-7092
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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Pred. No. 2.7e-154;
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                                                                                                                                               CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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APPLICANT:
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
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                                                                                            APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998 CLASSIFICATION:
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6300 Columbia Center,
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2.7e-154;
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                                                                                                                                          US-09-223-040-2
                                                                                                                                                                                      ; SOFTWARE: PatentIn Ver. 2
SEQ ID NO 2
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequ
                                                                                                                                                                                                                                                                      APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Myco
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009010US
FULL REPERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
SOPTWARE: Patentin Ver 7
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                                                                  Query Match
Best Local S
Matches 390
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                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 391 amino
TYPE: amino acid
STRANDEDNESS: sir
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142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                  Score 1944; DB 4;
pred. No. 1.7e-153;
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RESULT 6
US-08-818-112-111
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Query Match
                                                                                                               TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                             APPLICATION NUMBER: US/08/818
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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CITY: Seattle
STATE: Washing
                                                               STRANDEDNESS
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                                                 TOPOLOGY:
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 84.8%;
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                                                                                                                                                                                                  210121.411C6
Score 1652.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  701 Fifth Avenue
BB
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Length 396;
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US-08-818-111-106
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Patent No.
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                                        TELEPHONE: (206) 622-4
TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                               REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: W
                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 13-MAR CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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CITY: Seattle
LENGTH:
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                                                            (206) 682-6031
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ltive 19; Mismatches 34;
                                           106:
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Best Local Similarity
                                                                                                                                                 COUNTRY: USA

COUNTRY: USA

2 2 3 4 4 7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
CURRENT APPLICATION TOPOLOGY
APPLICATION NUMBER: US/09/056,556
TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                              ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 C
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                           Washington
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                                                                                                                                                                                                                                                                                                                                                                           6300 Columbia Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOUNDS AND METHODS
                                                                                                                                                                                     US/09/056,556
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                                                                                     210121.457
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Pred. No. 1.36
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Best Local Simi
Matches 337;
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                      APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                     STREET: 6300 Co
CITY: Seattle
STATE: Washing
                                                 APPLICATION NUMBER: FILING DATE: 05-MA
                                   CLASSIFICATION:
                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                    ADDRESSEE:
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TOPOLOGY: li
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Vedvick, Thomas S.
Twardzik, Daniel R.
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                                                 05-MAY-1998
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                                                                 US/09/072,596
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Pred. No. 1.3e-129;
                                                                                                                                                                                                                                                        701 Fifth Avenue
                                                                                                   Version
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TUBERCULOSIS

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RESULT 10
US-08-818-112-109
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Patent No. 62
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                     APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
CURRENT APPLICATION DATA:
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                                                                                                                  COUNTRY:
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                                                                                                                                  Washington
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                                                                                                                                                                     6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08818112
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                           Campos-Neto, Antonio
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Pred. No. 1.3e-1
9; Mismatches
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                   Version
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GENERAL INFORMATION:
APPLICANT: Reed, S
APPLICANT: Skeiky,
APPLICANT: Dillon,

Dillon, Davin C. Houghton, Raymond Vedvick, Thomas S. Campos-Neto, Antonia

Skeiky,

Steven

APPLICANT:
APPLICANT:

APPLICANT: Twardzik, Daniel R. TITLE OF INVENTION: COMPOUNDS AND

148

METHODS FOR DIAGNOSIS

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TUBERCULOSIS

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

E: SEED and BERRY LLP 6300 Columbia Center,

701

Fifth Avenue

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE:

PatentIn Release #1.0,

Version

#1.30

COUNTRY: CITY: Seattle ADDRESSEE:

USA

Washington

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US-08-818-111-104
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Sequence 104, Application US/08818111 Patent No. 6338852
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FILING DATE: 13 MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKL, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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Pred. No. 7.2e-
16; Mismatches
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RESULT 12
US-09-056-556-109
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US-08-818-111-104
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
ITTLE OF INVENTION: COMPOUNDS A.
NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                      Sequence 109, Application US/09056556 Patent No. 6350456
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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Local Similarity 84.2%;
nes 303; Conservative 10
                                                                                                                                                                              CITY: Seattle
STATE: Washing
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                                                                                                                                            ZIP: 98104-7092
                                                                                                                                                            COUNTRY:
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Pred. No. 7.2e-116;
6; Mismatches 36;
                                                                                                                                                                                                                701 Fifth
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RESULT 13
US-09-072-596-104
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 622-4900
                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                  APPLICANT:
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
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TELEPHONE: 1200
                                                                                                          CITY: Seattle
STATE: Washington
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
NVENTION: COMPOUNDS AND M
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                                                                                                                                       6300 Columbia Center,
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                                                                                             USA
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Dillon, Davin C.
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   PatentIn Release #1.0,
                                                                                                                                                            SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                 Steven G
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84.2%; Pred. No. 7.26
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   Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 91, Approximately No. 6290969
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                           APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 05-MAY CLASSIFICATION:
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6300 Columbia Center,
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Dillon, Davin C.
Campos-Neto, Antonio
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Pred. No. 7.2e-116;
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SEQUENCE CHARACTERISTICS:
LENGTH: 263 amin
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Best Local
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                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
         ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                     APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
                                                                                                                                                                          APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   APPLICANT:
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CURRENT APPLICATION DATA:
                                                                                                                                 STREET:
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STRANDEDNESS: sir
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                                                                                                  COUNTRY:
                                                                                                                                                               ADDRESSEE: SEED and BERRY LLP
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                                                                                                                Washington
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                                                                                                                                                 6300 Columbia Center,
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Dillon, Davin C.
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Pred. No. 3.9e-91;
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              Version #1.30
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APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Search completed: November 21, 2003, 17:06:38 Job time : 22 secs
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Result
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                             Score
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Match Length DB
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1949
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    /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
    /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
    /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
    /cgn2_6/ptodata/1/paa/US099_COMB.pep:*
    /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
    /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
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                                         Description
Sequence 102, App
                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                    STREET:
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RESULT 1
PCT-US99-03265-102
PCT-US99-03265-102
; Sequence 102, Application PC/TUS9903265
; GENERAL INFORMATION:
APPLICANT: COTIXA COTPORTATION
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVENTION: TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US99/03265
; FILING DATE: 17-FEB-1999
CLASSIFICATION: 435
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PCT-US99-03268-107
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Matches 391;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           COMPUTER READABLE FORM:
MEDIUM TYPE FLOOPY disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                    APPLICANT: CORIXA CORPORATION
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
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APPLICATION NUMBER:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9532-0023-228
                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 1949; DB 1; Local Similarity 100.0%; Pred. No. 1.7e-155; les 391; Conservative 0; Mismatches 0;
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                                                                                                           COUNTRY: USA
ZIP: 10036-2811
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                              Sequence 102, Application US/08658800 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND
NUMBER OF SEQUENCES: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Coruzzi, Laura, A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 95: TELECOMMUNICATION INFORMATION: TELEPHONE: 650-493-4935
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-FEB-1998
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                        CORRESPONDENCE ADDRESS:
                                    COUNTRY:
ZIP: 981
                                                                       CITY: Seattle
STATE: Washing
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TOPOLOGY: 1i
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FILING DATE: 17-FEB-1999
                                                                                                         STREET:
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                                                                                                                      ADDRESSEE:
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                                                                                                         6300 Columbia Center,
                                                        USA
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                                                                                                       701 Fifth Avenue
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US-08-659-683-107
US-08-659-683-107
US-08-659-683-107
Sequence 107, Application US/08659683
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
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FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Waki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acids
STRANDERNESS: sincle
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COMPUTER READABLE FORM:
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                                                                          STREET: 6300 C
                    COUNTRY: USA
ZIP: 98104-7092
                                                                                                                ADDRESSEE: SEED and BERRY LLP
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                                                                                            6300 Columbia Center,
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SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
TITLE OF INVENTION: COMPOUNDS AN
NUMBER OF SEQUENCES: 128

AND

METHODS

FOR DIAGNOSIS

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TUBERCULOSIS

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center,

701 Fifth

CITY: Seattle

Washington

COUNTRY: USA TTP: 98104-7092

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US-08-680-573-102; Sequence 102, Application US/08680573; GENERAL INFORMATION:
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Best Local 8
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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ACTERISTICS:

AS 391 amino acids

ASTRANDEDNESS:

TOPOLOGY:

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659-683
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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/659,683

FILING DATE: 05-JUN-1996
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622.4900
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NAME: MAKL, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                    Sequence 107, Application US/08680574 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,573
FILING DATE: 12-JUL-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
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LENGTH: 391 amino acids
                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 133
                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
  CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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STRANDEDNESS: sin
                                    STREET:
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                                    6300 Columbia Center,
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                                      701 Fifth Avenue
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                                                                                                                                                                                                                            RESULT 7
US-08-729-622-102
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                                                                                                                                                                                      Sequence 102, Application US/08729622 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680
FILING DATE: 12-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A
APPLICANT: Dillon, Davin C
APPLICANT: Campos-Neto, An
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  TITLE OF INVENTION:
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ZIP: 98104-7092
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                            Houghton, Raymond
Vedvick, Thomas H.
Twardzik, David R.
VENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                              Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                              Campos-Neto, Antonio
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TUBERCULOSIS
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180 180

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Sequence 107, Applicati
GENERAL INFORMATION:
APPLICANT: Reed, St
APPLICANT: Skeiky,
APPLICANT: Dillon,
APPLICANT: Campos-N
                                                                                                                        RESULT 8
US-08-730-510-107
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PstentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,622
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 622-4900
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LENGTH: 391 amino acids
TYPE: amino acid
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                                                                                                         Application US/08730510
               Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
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INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amin^ ---
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Best Local Similarity 100.
Matches 391; Conservative
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APPLICATION DATA:
APPLICATION NUMBER: US/08/730
FILING DATE: 27-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
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APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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ZIP: 98104-7092
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RESULT 9 US-08-942-341-102

Sequence 102, Application US/08942341 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILING DATE: 01-OCT
CLASSIFICATION: 435
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                   GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                  LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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US-08-942-578-107
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Best Local Similarity
Matches 391; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/942
FILING DATE: 01-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Washing
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                                                                            MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                     LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                  MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                   LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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E: SEED and BERRY LLP 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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                                                                                                                                                                                                                                                                                                                                                                                     Score 1949; DB 13;
Pred. No. 1.7e-155;
D; Mismatches 0;
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RESULT 11
US-09-024-753-102
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Best Local S
Matches 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,753
FILING DATE: 18-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                              Local Similarity
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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
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                                  LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                              LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 amino acids
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6300 Columbia Center,
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Dillon, Davin C.
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US-09-025-197-107
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
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                                                                                                                                                                                                       Matches 391;
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Best Local
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APPLICANT: Twardzik,
APPLICANT: Lodes, Mid
TITLE OF INVENTION: 0
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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TOPOLOGY: lir
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SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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Dillon, Davin C.
Campos-Neto, Antonio
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linear
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Pred. No. 1.7
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1.7e-155;
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US-09-072-967-107
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SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION: TARCHUMENT OF THE CONTROLLED OF 
                                                                                                                    Matches
                                                                                                                                               Query Match
Best Local (
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, For Invention: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
TUBER OF SEQUENCES: 355
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CITY: Seattle
STATE: Washington
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MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                              MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Vedvick, Thomas S.
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                                                                                                           100.0%; Score 1949; DB 14; 100.0%; Pred. No. 1.7e-155; tive 0; Mismatches 0;
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; FEATURE:
7 OTHER INFORMATION: MTB39 (TbH9) protein full-length
US-09-597-796C-8
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PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
PRIOR PILING DATE: 1998-12-30
PRIOR PILING DATE: 1999-04-07
PRIOR PPLICATION NUMBER: WO PCT/US99/07717
PRIOR APPLICATION NUMBER: WO 90/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 60/158,338
PRIOR PILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: US 60/158,338
PRIOR PILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: US 60/158,425
PRIOR FILING DATE: 1999-10-07
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                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver.
SEQ ID NO 8
LENGTH: 391
                                                                                                                                                                                                                                                Matches 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009050US
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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121 LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
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Pred. No. 1.7e-155;
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APPLICANT: Reeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Houghton, Raymond L.
APPLICANT: MONEIL, Patricia D.
APPLICANT: MONEIL, Patricia D.
APPLICANT: Lodes, Michael L.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009041US
CURRENT APPLICATION NUMBER: US/09/688,672A
CURRENT APPLICATION NUMBER: US 60/158,338
PRIOR APPLICATION NUMBER: US 60/158,338
PRIOR APPLICATION NUMBER: US 60/158,425
PRIOR APPLICATION NUMBER: US 60/158,425
SPRIOR FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: US 60/158,425
SPRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 202
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 26
LENGTH: 391
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: TbH9 (Mtb39A)
US-09-688-672A-26
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US-09-688-672A-26
; Sequence 26, Application US/09688672A
; GENERAL INFORMATION:
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Search completed: November 21, 2003, 17:09:44
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Result
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Q10813;
Q1-OCT-1996
15-DEC-1998
16-OCT-2001
                                                                                                                                MEDLINE=98295987; PubMed=9634230; Gornier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Stelton S., Squares S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical PPE-family protein Rv289;
RV2892C OR MT2959 OR MTCY274.23C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYCTU
         STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ernolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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CONFLICT 1
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RESULT
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TI02_MYCTU STANDARD; PRT; 463 AA. 053951; Ocreated) 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical PPE-family protein Rv1802. PRV1802 OR MY1851 OR MYV049.24.

RV1802 OCR MY1851 OR MYV049.24.

Mycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacteridae; Act

Mycobacterium

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Matches 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
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EMBL; AE007119; AAK47285.1; --
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Pfam; PF00823; PPE; 1.
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394
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182; Conser
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YGFRLAVMORPPFAG
                                                                                                                                                               VPQAWAAANQAVTPAARALP---LTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VATNFFGQNTPAIAATEAQYAEMWAQDAAAMYAYAGSAAIAT-ELTPFTAAPVTTSPAAL
                                                    VPPRPYVMPHSPAAG
                                                                                                             VPPDWAARARWANPAAWRLPGDDVTALRGTAENA---LLRGFPMASAGQSTGGGF--VHK
                                                                                                                                                                                                                                                                             QAVQTAAQNGVRAMSSL--GSSLGS----
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41.8%;
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Pred. No. 4.4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Kolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome. CONFLICT 401 401 S -> L (IN SEQUENCE 463 AA; 46021 MW; EE64828BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TubercuList; Rv1802;
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL022021; CAA17723.1; EMBL; AE007044; AAK46123.1;
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                                    NSMLGLGFAESKMVLPANDTVISTIFGMVQFQKFFNPVTPFNPDLIPK-------
                                                                                                                                                  LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI-
                                                                                                                                                                                        AATNIFGONTGAIAAAEARYAEMWAQDAAAMYGYAGSSSVAT-QVTPFAAPPPTTNAAGL
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                                                                                                                ATOGVAVAQAVGASAGN-ARSLVSEVLEFLA--TAGTNYNKTVASLMNAVTGVPYASSVY
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·SSGLGG----GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPL
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Pred. No. 4.5e-33;
8; Mismatches 136;
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EE64828BF09FA551 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                          136; Indels
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr: Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr: Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Barcell T., Gentles S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Mature 393:537-544 (1998).
                                                                                                                                                                               between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                laboratory strains.";
Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRALN=CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg;

Kolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula J.,

Peterson M., Utterback T., Weidman J., Khouri H., Gill J., Mikula J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P4261; O53727;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Hypothetical PPE-family protein Rv0442c.
RV0442C OR MT0458 OR MTV037.06C.
                                                                 EMBL; M15467; AAA68235.1; ALT_INIT.
EMBL; ALCO1932; CAA17399.1; --
EMBL; AECO6948; AAK44681.1; --
PIR; C70830; C70830.
TIGR, MT0458; --
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a copyred the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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InterPro; IPR000030; Microbac PPE.
InterPro; IPR002989; Mycobac pentapep.
Pfam; PF01469; Pentapeptide_2; 5.
                                                      TubercuList; Rv0442c;
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Bacteriol. 169:1080-1088(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=3029018;
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                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis clinical and
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complete
Nature 39
[2]
                                            MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavier R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv0878C.
RV0878C OR MT0901 OR MTCY31.06C.
                                                                                                                                                                                                                                                                                                                                                     STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonar A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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TubercuList; Rv0878c;

    -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
    -!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.

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STRAIN=CDC 1551 / Oshkosh;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Z73101; CAA97385.1; -.; AE006977; AAK45143.1; C70780; C70780.
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                                                                                                                                                                                                                                                                                                                                                                                                              Pro; IPR000030; Microbac_PPE.
Pro; IPR002999; Mycobac_pentapep
PF01469; Pentapeptide_2; 4.
PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                     LSLVLSNLFGQNLPAIAATEASYEQLWAQDVAAMVGYHGGASTVASQLTPWQQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGPAAAAMAAAAAPYLSWLNAATARAEGAAAGAKAAAAVYEAARAATAHPALVAANRNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNFMVLPPEVNSARIYAGAGPAPMLAAAVAWDGLAAELGMAAASFSLLISGLTAGPGSAW
                                            RALPLTSLTSAAERGPGQMLGGL--PVGQMGARAGGGLSG
                                                                                                                                                                                        GNFLGIGNIGNNNVGSGNTGDYNFGIGNIGNANLGNGNIGNANLGSGNAGFFNFGNGNDG
                                                                                                                                                                                                                                       SNMV---SMANNHMSMTNSG------VSMTN-----TLSSMLKGFAPAAAAQAV
                                                                                                                                                                                                                                                                                    --LLSVLPPVVTAAPAGAV-----GVPAA---LAIPALGV---ENIG------V
                                                                                                                                                                                                                                                                                                                                   GGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAEL
-----TNTGGFNSGDLNTGIGSPVTQGVANSGFGNTG
                                                                                              NTNFGSGNAGFLNIGSGNEGSGNLGFGNAGDDNTG-
                                                                                                                                      QTAAQNGVRAMSSLGS-SLGSSGLGGGVAA--NLGRAASVGSLSVPQAWAAANQAVTPAA
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38 59 79
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181 21
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POTENTIAL.
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Pred. No. 5.
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4 X 10 AA APPROXIMATE REPEATS; C58BEC607F0675E2 CRC64;
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RESULT 6
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Q10778;
01-OCT-1996
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYCTU
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Pfam;
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Submitted (APR-2001) to the
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16-OCT-2001 (Rel. 40, Last annotation updat
Hypothetical PPE-family protein Rv1548c.
RV1548C OR MT1599 OR MTCY48.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A70762; A70762.
TIGR; MT1599; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z74020; CAA98335.1; -. EMBL; AE007026; AAK45866.1;
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TRANSMEM
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    !- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro; IPR000030; Microbac_PPE.
Pro; IPR002989; Mycobac_pentapep.
PP01469; Pentapeptide_Z; 11.
PF00823; PPE; 1.
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SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                         MNFSVLPPEINSALMFAGAGPGPMLAAASAWTGLAGDLGSAAASFSAVTSQLATGSWQGP
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14 34 POTENTIAL.
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258 D
66736 MW;
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                                                                                                                                                                                                 Score 418;
Pred. No. 2.
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D -> G (IN REF.
                                                                                                                                                                                                                                                                                        -> G (IN REF. 2).
209F1593D52533A2 CRC64;
                                                                                                                                                                           Mismatches
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FRO SEQUE

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RA THOM

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Q07297;
Q1-NOV-1995
Q1-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                MEDLINE-21/18732; PubMed=11234002;

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vega-Lopez F., Brooks L.A., Dockrell H.M., de Thompson J.K., Hussain R., Stoker N.G.; "Sequence and immunological characterization from Mycobacterium leprae."; Infect. Immun. 61:2145-2153(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRA OR MI0411 OR MLCL383.14.
Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                     "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                 Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A Mycobacterium leprae-specific gene recognized 45 kDa protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rinke de Wit T.F., Clark-Curtiss J.E., Jonson A.A.M., Thole J.E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
antigen (251) (45 kDa protein).
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PIR; S33522; S33522.
PIR; S39872; S39872.
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                                                                             -WYCTU STANDARD; PRT; 463 AA. Q10892; Q10892; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical PPE-family protein Rv0096.
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EMBL; X68431; CAA46480.1; --
EMBL; Z21952; CAA79950.1; --
EMBL; Z97179; CAB09938.1; --
EMBL; AL583918; CAC29919.1;
                                       Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                      Corynebacterineae; Mycobacteriaceae;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Integral membrane protein (Pot

-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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TubercuList; Rv0096;
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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EMBL; AE006922; AAK44327.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White U., Fleischmann R.D., Alland D., Ewinn M.L., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Salzberg S.L. Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Kolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula A., Nelson W.C., Weidman M.C., Weidman M., Nelson W.C., Weidman M., Nelson W.C., Weidman M., Nelson W.C., Weidman M., Weidman M., Weidman W.C., Weidman M., Weidman M., Weidman W.C., 
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COle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Bevlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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P31500; O53265;
O1-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence updated)
28-FEB-2003 (Rel. 41, Last annotation upon the sequence of the seque
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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(See http://www.isb-sib.
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Best Local S
Matches 115
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TIGR; MT3098; -
TIGR; MT3101; -
MEDIINE-88295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr:
Cole S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyc
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                           O53268; O53269;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Hypothetical PPE-family protein Rv3021c/Rv3022c.

RV3021C/RV3022C OR MT3106 OR MTV012.35C/MTV012.36C.
                                                                                                                                                                                                                                                                                                                                                                                                         MYCTU
                                                                                                                                                            STRAIN=H37Rv;
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; SEQUENCE 434 AA; 43
                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  Corynebacterineae; Mycobacteriaceae; Mycobacterium
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; AE007129; AAK47427.1; ALT_SEQ.
;; AE007129; AAK47430.1; ALT_SEQ.
;; X59271; CCAA41961.1; ALT_FRAME.
E70857; E70857.
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3029 MW; 41D673C4BD389DD6 CRC64;
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Pred. No. 4.7e
56; Mismatches
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4.7e-12;
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                                                                                                                          Harris
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Matches
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Best Local
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TubercuList; Rv3021c; -. TubercuList; Rv3022c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-i- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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EMBL; AL021287; CAA16107.1; ALT_FRAME.
EMBL; AE007129; AAK47435.1; -.
TIGR; MT3106; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: Ref.1 sequence
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361
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hetical protein; Complete proteome.
ICT 299 29 G -> A (IN
ICT 317 320 LAGV -> VIC
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                                                                                                                                      LAILSIGWIISNIFGAIPVLGGPLLGALAAAVVPGVAGLAGVAGLAALPAVGAAAGAP--
                                                                                                                                                                                  MSMTNSGVSMTNTLSS-----MLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGL
                                                                                                                                                                                                                                                                               QLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSM----
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GOMGARAGGGLSGV
                                                                                     GGGVAANLGRAASV-GSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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42876 MW;
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LAGV -> VTGL (IN REF.
L -> V (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 321.5; DB 1;
Pred. No. 6.6e-12;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Ha:
Cole S.Y., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holro
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
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006246;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upo
16-OCT-2001 (Rel. 40, Last annotation upo
19-pothetical pps_family protein Rv3429
RV3429 OR MT3533 OR MTCY77.01.
                                                                                                                                                                                       InterPro; IPR000030; Microbac_PPB
Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete pro
                                                                                                                                                                                                                                                                                     EMBL; Z95389; CAB08678.1; -
EMBL; AE007158; AAK47873.1;
                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
under the by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to
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Kolonay J.F., Nelson W.C., Umayam L.A., Ermol
Delcher A., Utterback T., Weldman J., Khouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
Bacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                     TubercuList; Rv3429; -
                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison
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                  60
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                                                                                                             65;
                                                                                                                            Similarity
GSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELM
                                                                    LPPEINSARMYAGPGSASLVAAAQ----MWDS---VASDLFSAASAFQSVVWGLTVGSWI
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                                               IPAEYISNIIYEGPGADSLSAAAEQLRLMYNSANMTAKSLTDRLGELQE-----NWK
                                                                                                             Conservative
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19811 MW; 8BE1FC025ABFBEA6 CRC64;
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Pred.
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                                                                                                             Mismatches
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Gwinn M.L., Haft D., Hickey
L.A., Ermolaeva M.D., Salzbe
J., Khouri H., Gill J., Miku
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.3e-07;
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Best Local :
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COle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:337-544(1998).
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Q50703;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv3425.
RV3425 OR MTCY78.04C.
                                                                                                                                                                                                                                                                            Pfam; PF00823; PPE;
Hypothetical protei
SEQUENCE 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                           Similarity
AGVNTPAIADLDAQYDQYRARNVAVMNAYVSWTRSALSDLPRWREPPQIYRGG
                              LGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLLPFEEAPEMTSAG
                                                                   ADAVERYLOWLSKHSSOLKHAAWVINGLANAYNDTRRKVVPPEEIAANREERRRLIASNV
                                                                                                 VAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNL
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176 AA; 19
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                                                                                                                                                                                                                                                                      1; Complete proteome.
19855 MW; B8CEF2E9463B87B0 CRC64;
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                                                                                                                                                                                                                           11.2%; Score 217.5; 33.5%; Pred. No. 2.
                                                                                                                                                                                                         31; Mismatches
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                                                                                                                                                                                                         83;
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ELS_MOUSE
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Matches 115
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01-OCT-1996
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MEDLINE=95130069; PubMed=7829060;
MYDDAINE=95130069; PubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin mouse chromosome 5 in a region of linkage conservation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA /
NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLI-
-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGET!
INTO AN EXTENSIBLE 3D NETWORK.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Elastin precursor (Tropoelastin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 7.";
Genomics 23:125-131(1994).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                     492
                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                              460 YGVGAGAGL -- GGASPAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                     402 GGIPGVGGPGIGGPGIVGGPGAVSPAAAAKAAKA--YGARGGVGIPTYGVGAGGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115;
                                                                                                                                                                                                                                                                                                                                                                              59 -- IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GALP----PEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                   LMNNVPQALQQLAQPTQGT---
                                                                                                                                                               TSAGGL----
                                                                                                                                                                                                                  ALGGLVPGAVPGAVPAVPGAGGVPGAGTPAAAAAAAAAAAAAAKAGLGPGVGGVPGG
                                                                                                                                                                                                                                                                     ELMILIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLP-FEEAPEM
LGAGVPGFGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGAVPGSLAASKAAK
                                                                                                      VGVGGIPGGVGVGGVGGGVGPGGVTGIGAGPGGLGGAGSPAAAKSAAKAAAKAQYRAAAG
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71955 MW;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COBESAABIEDD7F1 CRC64;
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                                                   --- TPSSKLGGLWKTVSPHRSPISNMVSMANN
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                                                                                                                                                            ----LEQAAAVEEASDTAAANQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Last seque 16-OCT-2001 (Rel. 40, Last annot Hypothetical PPE-family protein RV3426 OR MTCY78.03C.
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                                                                                                                                                                                                                                                                                                                             Pfam; PF00823; PPE; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 232 AA; 25872 MW; D76512D49EB272C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
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TubercuList; Rv3426;
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                                                                  ADAALRYLDWLSKHSRQILRTARVIESLVMAYEETLLRVVPPATIANNREEVRRLIASNV
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                                                                                                                                                      I PAEYI SNVI YEGPRADSL YAADQRLRQLADSVRTTAESLNTTLDELH-ENWKGSSSEWM
                                                                                                                                                                                                                                             Conservative
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35.2%;
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ly protein Rv3426.
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                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                        Score 151.5; DB Pred. No. 0.022; 8; Mismatches
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Elastin prec
                 EMBL;
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or send an email to license@isb-sib.ch).
                                                                                                           the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
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-!- FUNCTION: MAJOR STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92241859; PubMed=1572637;
Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.
"Elements of the rat tropoelastin gene associ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd "Rat tropoelastin is synthesized from a 3.5-kilobase J. Biol. Chem. 263:13504-13507(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91104868; PubMed=1702999;
Pierce R.A.; Deak S.B., Stolle C.A.,
"Heterogeneity of rat tropoelastin m
Biochemistry 29:9677-9683(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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Mammalia; Eutheria;
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splicing."
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SUBUNIT: THE POLY
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                                                                                                                                                                                                                                                                Name=8;
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Event-Alternative splicing; Nameo re
M60647;
J04035;
M86372;
                                                                                                                                                                                                                                                                              IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246,
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M: THE CROSSLINKS
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-2003 (Rel.
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 AAA42269.1;
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AAA42271.1;
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42, Last annotation update)
(Tropoelastin) (Fragment).
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND ALTERNATIVE
                                                                                                                                                                                                                         Sequence=VSP_004244, VSP_004245, VS ARE MADE OF DEAMINATED LYS.
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Matches 102;
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EMBL; M86363; AAA42271.1; JOINED.
EMBL; M86364; AAA42271.1; JOINED.
EMBL; M86366; AAA42271.1; JOINED.
EMBL; M86371; AAA42271.1; JOINED.
EMBL; M86375; AAA42272.1; JOINED.
EMBL; M86373; AAA42272.1; JOINED.
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VARSPLIC 263 307
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PRINTS; PR01500; TROPOELASTIN.
Structural protein; Connective tissue; Repeat; Signal;
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                                                                              342 SLTSAAERGPGQMLGGLPVGQMGARAG-GGLSGV 374
                                                                                                                                                                                                                                                                                                        117 ELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMT 176
                                                                                                                                                                                                                                                                                                                                  457 YGVGAGAGL------GGASQAAAA----AAAAKAAKYGAG------
                                                                                                                                                                                                                                                                                                                                                                                         399 GGIPGVGGPGIGGPGIVGGPGAVSPAAAAKAAKAAK--YGARGGVGIPTYGVGAGGFPG 456
                                                                                                                                                                                                                                                                                                                                                           59 --IGSSAGIMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGITVPPPVIAENRA 116
                                                                                                                                                                                                                                                                                                                                                                                                                    5 GALP----PEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSW--
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                                                                                                                                   SLGSSLGSSGLGGGV-----AANLGRAASV---GSLSVPQAWAAANQAVTPAARALPLT 341
                                                                                                                                                                                         PHRSPISNMVSMANNHMSMTNSGVSM-TNTLSSMLKGF-APAAAAQAVQTAAQNGVRAMS
                                                                                                                                                                                                                      SAGGLL---EQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSS-KLGGLWKTVS 232
                                                                                                                                                               PG------GVTGIGTGPGTGLVPGDLGGAGTPAAAKSAAKAAAKAQYRAAA
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;; Pred. No. 0.11;
31; Mismatches 153
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BY SIMILARITY.
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Title:
Perfect score:
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Maximum Match 100%
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     SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numan:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
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1949
1 MVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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667.5	668.5	675	682.5	683.5	702	702	731	736	737.5	751	754	779.5	1583	1648	1949	Score	
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050378	P95249	053393	Q8VJX6	065937	Q8VJ65	P71862	053949	Q8VKN2	007232	050424	006206	050379	053722	006304	Q8VKM3	Q8VJK7	P95247	033205	P71869	005798	005907	Q8VKL9	033312	Q9AGF0	Q8VJW5	086373	053940	0SVJZ0
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ALIGNMENTS

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Hypothetical 39.2 kNa protein (PPE lamily protein). RV1196 OR MTC1364.08 OR MT1234. Mycobacterium tuberculosis. Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCB1_TaxID=1773; SEQUENCE FROM N.A. STRAIN=H37RV; SEQUENCE FROM N.A. STRAIN=H37RV; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Cole S.T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; [2] Nature 393:S37-544(1998). [2] REDIENCE FROM N.A. STRAIN=CDC 1551 / Oshkosh; Feleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.	01-JUL-1997 (TrEMBLrel. 04, Created) 01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)	LT 1 98 005298 PRELIMINARY; PRT; 391 AA.

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EMBL; AE007000; AAK45;
TIGR; MT1234; -.
TubercuList; Rv1196;
PROSITE;
                                                                                                                                                                                           laboratory strains.";
submitted (APR-2001) to the
EMBL; AE007161; AAK47941.1;
                                                        InterPro; IPR000030; Microbac PPE InterPro; IPR000508; SigPTase. Pfam; PF00823; PPE; 1.
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Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe
Kolonay J.F., Utterback T., Weidman J., Khouri H., Gill J., Miku
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STRAIN=CDC 1551 / Oshkosh;
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Mycobacterium tuberculosis
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   PS00501; SPASE I 1; 1
393 AA; 39688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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E409396B3ABDC0F8 CRC64;
      86F0B67798855511 CRC64;
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J., Mikula
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Best Local Simi
Matches 335;
                                                                                                                                     MEDLINE=99295987; PubMed=9634230;

A COle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Har A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holro A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L. A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Tomplete genome sequence.";

T Complete genome sequence.";

Nature 393:537-544(1998).
             Query Match
Best Local :
Matches
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein Rv3478.
RV3478 OR MTCY13E12.31.
                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacte
Corynebacterineae; Mycobacteriaceae;
                                                        Hypothetical SEQUENCE 3:
                                                                                                             EMBL; Z95390; CAB08702.1; -. TubercuList; Rv3478; -.
                                                                                                                                                                                                                                                                                                                  STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                  Pro; IPR000030;
PF00823; PPE; 1
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                                                      1 protein; Com
393 AA; 39413
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             81.2%;
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                                                      Complete | 19413 MW;
                                                                                              Microbac_PPE
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Pred.
             Score 1583;
Pred. No. 1
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AF4C20C95DAE7DD4
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No. 4.3e-84;
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, Murphy L.,
Rogers J.,
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37;

Gaps

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121

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laboratory strains.";
Submitted (APR-2001) to the E
EMBL; AL0022021; CAA17711.1; A
EMBL; AE007043; AAX46108.1; -
TIGR; MT1838; -
TubercuList; Rv1789; -
                                                                                                                                                                                                                                                                                                                       MEDLINE-98295987; PubMed=9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A.,
Fleischmann R.D., Dodson R., Gwinn I
Peterson J., DeBoy R., Dodson R., Gwinn I
Kolonay J.F., Nelson W.C., Umayam L.A., I
Delcher A., Utterback T., Weidman J., Kh
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01-MAR-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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RV1789 OR MT1838 OR MTV049.11.
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                                                                                                                                          "Whole genome comparison of
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Matches 179
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Q99QI1;
01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, L
01-OCT-2002 (TrEMBLrel. 22, L
Rv1808-like protein.
MYC1808 OR OV1808.
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Sivadon V., Heym B., Mazancourt P., Gaillard J
"PPE Rv1808 orthologue of Mycobacterium microt
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ
EMBL; AF335180; AAK20894.1; -
EMBL; AF335179; AAK20893.1; -
InterPro; IFR000030; Microbac PPE.
                                                                                                                                                                                                                                         InterPro; IPR000030; Pfam; PF00823; PPE; SEQUENCE 410 AA;
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Complete proteome.
SEQUENCE 411 AA;
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44.5%; Pred. No. 2e-34;
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Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O. Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikul
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                          Pro; IPR000030; PF00823; PPE; :
                                                                                                                                                                                                                                                                                      AL022021; CAA17729.1;
AE007044; AAK46129.1;
                                                                                                                                                                                                                                                              MT1856.1;
                                Similarity
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Last sequence update)
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                                                                                                                                                                                                                                                                                ALT_INIT
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                             Score 751;
Pred. No. 2
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
I Nature 393:537-544(1998).
                                                                                                                                                                                                                             STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eiser
Fleischmann R.D., Alland D., Eiser
Rolerson J., DeBoy R., Dodson R.,
Kolonay J.F., Nelson W.C., Umayam
Delcher A., Utterback T., Weidman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                   laboratory strains.";
Submitted (APR-2001) to the
EMBL; AL022021; CAA17728.1;
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RV1807 OR MT1856 OF
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                MT1856;
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, Gwinn M., Haft D.
m L.A., Ermolaeva N
n J., Khouri H., Gi
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M., Haft D., Hickey E
Ermolaeva M., Salzber
houri H., Gill J., Mi)
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CONFLICT 227
CONFLICT 238
SEQUENCE 403 AA;
complete
Nature 39
[2]
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O1.-JUN-1998 (TrEMBLrel. 06, Created)
O1.-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1.-JUN-1998 (TrEMBLrel. 22, Last annotation update)
PPE-family protein (PPE family protein).
RV1801 OR MTW049.23 OR MT1850.
                  MEDLINE-9829987; PubMed-9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gardon S.V., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Chillingworth T., Connor R., Walles R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria, Actinobacteria, A
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Matches 182
                                                                                                                                                                                                      Q9Z5KO PRELIMINARY; PRT; 421 AA.
Q9Z5KO;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative PPE protein (PPE-family protein).
ML1182 OR MLCB1701.08C.
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
laboratory strains.";
Submitted (APR-2001): to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17722.1; -.
EMBL; AE007044; AAK46122.1; -.
                                                                                                    Corynebacterineae;
NCBI_TaxID=1769;
                                                                                                                                                             Mycobacterium leprae.
Bacteria; Actinobacteridae;
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TubercuList; Rv1801; -.
TubercuList; Rv1801; Microbac_PPE.
                                                      SEQUENCE
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Fam; PF00823; PPE; 1
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Pred. No. 2.
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MEDLINE=21128732; PubMed=11234002;

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P96362
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                                                                                                                                                                                                                                                                     P96362;
P96362;
01-MAY-1997
01-MAY-1997
01-OCT-2002
                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 38.1 kDa protein (PPE family protein).
RV1039C OR MTCY10G2.10 OR MT1068.
SEQUENCE FROM N.A. STRAIN=H37RV; MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.", hature 409:1007-101(2001).
EMBL, AL049191; CAB39148.1; -.
EMBL; AL583921; CAC31563.1; -.
                                                                                                       NCBI_TaxID=1773;
                                                                                                                                     Bacteria; Actinobacteria;
Corynebacterineae; Mycobac
                                                                                                                                                                                         Mycobacterium tuberculosis
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        PubMed=9634230;
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Pred. No. 3.9e
55; Mismatches
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O06386; 01-JUL-1997 (01-JUL-1997 (01-OCT-2002 (Hypothetical RV3621C OR MT

7 (TrEMBLrel. 04, Created)
7 (TrEMBLrel. 04, Last sequence update)
2 (TrEMBLrel. 22, Last annotation update)
al 40.7 kDa protein (PPE family protein).
MTCY15C10.31 OR MTCY07H7B.01 OR MT3723.

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Best Local Simi
Matches 166;
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Fleischmann R.D., Alland D., Eisen
Fleischmann R.D., Alland D., Eisen
Roterson J., Debby R., Dodson R.,
Kolonay J.F., Nelson W.C., Umayam
Delcher A., Utterback T., Weidman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F. Badcock K., Basham D., Brown D., Chillingworth TI., Connor R. Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hchornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J. Rutter S., Seeger K., Skelton S., Squares R., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.", Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Z92539; CAB06873.1; -.
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STRAIN=CDC 1551 /
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356
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                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                        SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
VTGMMP-GMASAAKGTGAYAGPRYGFKPTVMP
                             MLGGLPVGQMGARAGGGLSGVLRVPPRPYVMP
                                                                            SSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQ
                                                                                                                                                                                          VATNVLGINTPAIMATEALYAEMWAQDALAMYGYAAASG-AAGMLQPLSPPSQTTNPGGL
                                                                                                                                                                                                                                                      IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                          ASMAMVAAAQPYLAWLTYTAEAAAHAGSQAMASAAAYEAAYAMTVPPEVVAANRALLAAL
                                                                                                                                                                                                                                                                                                                                                        MDFGALPPEINSARMYAGAGAGPMMAAGAAWNGLAAELGTTAASYESVITRLTTESWMGP
                                                                                                                 TPFVANIINSAVNTAAWYVNAAIPTAIFLANALNSGAPVAIAEGAIEAAEG---AASAAA
                                                                                                                                             P--ISMMVSMANNHMS-MTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLG
                                                                                                                                                                          AAQSAAVGSAAATAAVNQVSVADLISSLPNAVSGLASPVTSVLDSTGLSGIIADIDALLA
                                                          AGLADSVTPAGLGASLGEATLVGRLSVPAAWSTAAPATTAGATALEGSGWTVAAEEA-GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           il protein;
391 AA; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38081 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
8081 MW; AFDF3EA4FB195C4F
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 702; DB 16;
Pred. No. 1.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Gwinn M.L., Haft D., Hicky
L.A., Ermolaeva M.D., Salzbe
J., Khouri H., Gill J., Miku
386
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                                                                                                                                                                                                                                                                                                                                                                                                                 150;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
SEQUENCE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE007171; AAK48084.1; -. TIGR; MT3723; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains.";
Submitted (APR-2001) to the
EMBL; 295436; CAB08826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonar A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TubercuList; Rv3621c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterineae; Mycobacteriaceae; Mycobacterium
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
Bacteria; Actinobacteria; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000030; Microbac_PPE
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                             382
                                                                                                                                                                                                                                                                                                                                                       180
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    YVMPHSPAAG
|: || |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATATLLPFEEAPEMTSAGG
                                                                        WTATTPAASPAVLAASNGLGAAAAAEGSTHAFGGMPL--MGSGAGRAFNNFAAPRYGFKP
                                                                                                                 WAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVL--RVPPRP
                                                                                                                                                                  YFGLAHDLPKWASEGAKAAGEAAKALPAAVPAIPSAGL-SGVAGAVGQAASVGGLKVPAV
                                                                                                                                                                                                                                                         ALGLTGHTWSSDGSGLIVGGVLGDFVQGVTGSAELDASVAMDTFGKWVSPARLMVTQFKD
                                                                                                                                                                                                                                                                                                       MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA---AAQAVQT-----
                                                                                                                                                                                                                                                                                                                                                                                              LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                               LLATNFLGQNTAAIAATEAQYAEMWAQDAAAMYGYAGASAAAT-QLSPFNPAAQTINPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSAASMVAAATPQVAWLRSTAGQAEQAGSQAVAAASAYEAAFFATVPPPEIAANRALLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLDFAQLPPEVNSALMYAGPGSGPMLAAAAAWEALAAELQTTASTYDALITGLADGPWQG
                                                                                                                                                                                                                                                                                                                                                   LASQAASVGQAVSGAANAQALTDIPKAL-----FGLSGIFTNEPPWLTDLGK
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413 AA; 4
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0679 MW; DAAFE8917A3900A3 CRC64;
                                                                                                                                                                                                           AAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQA
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RESULT
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AC 05
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AC QBUJWO;
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COC MCDI-TA
RN (1)-NC
RD SEQUENC
RC STRAIN=
RA Peterso
RA Fleisch
RA Peterso
RA CIONAY
RA Delcher
RA Peterso
RA CIONAY
RA Delcher
RA Fleisch
RA TIGR;
MHOle
RT Laborat
RI Submitt
DR Interpr
DR SEQUENC
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Best Local S
Matches 166
O53958;
O53958;
O1-JUN-1998
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01-MAR-2002
01-MAR-2002
01-MAR-2003
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Peterson J., DeBoy R., Dodson R., Gwinn N
Kolonay J.F., Nelson W.C., Umayam L.A., E
Delcher A., Utterback T., Weidman J., Kho
Bishai W.
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
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Bacteria, Actinobacteria, A
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InterPro; IPR000030; Microbac_PPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                            13
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694 AA; 73206 M
                                                                                                                                                                                        AVTPAARALPLTSLTSA-AERGPGQMLGGLPVGQMGARAGGGL
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                                                                                                                                                               AVRLVANTLPATSLAAAPATQIPANLLGOMALGSM----TGGAL
                                                                                                                                                                                                                                                                                                    AQAVQTAAQNGVRAMSSLGSSLG-----SSGLGGGVAANLGRAASVGSLSVPQAWAAANQ
                                                                                                                                                                                                                                                                                                                                                   IFGPTGATTYQNLFVTA----ANVTKFSTWANDAMSAPNLGMTEFKVF-----WQPPPA
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  (TrEMBLrel.
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                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n J.A., Carpenter L., White O.,
Gwinn M.L., Haft D., Hickey E.,
L.A., Ermolaeva M.D., Salzberg
J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium
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465 216 405 181 121

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RESULT 14
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. A Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekaia F., A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
L. Nature 393:537-544(1998).
EMBL; AL022021; CAA17730.1; -.
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Best Local &
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              P95190;
P95190;
01-MAY-1997
01-MAY-1997
01-OCT-2002
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InterPro; IPR000568;
InterPro; IPR000030;
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Bacteria; Actinobacteria; Actinobacte
Corynebacterineae; Mycobacteriaceae;
 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RV1809 OR MTV049.31.
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01-MAR-2003
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PROSITE; PS00449; ATPASE_A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                VATNIFGQNTAAIAATEAEYGEMWAQDTWAMFGYASSGATA-SRLTPFTAPPQTTNPSGL
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                                                                                                                                                    RLVANTLPATSLAAAPATQIPANLLGQMALGSM---TGGAL
                                                                                                                                                                               TPAARALPLTSLTSA-AERGPGQMLGGLPVGQMGARAGGGL
                                                                                                                                                                                                                                             AVQTAAQNGVRAMSSLGSSLG-----SSGLGGGVAANLGRAASVGSLSVPQAWAAANQAV
                                                                                                                                                                                                                                                                          NAIFGPTGATTYONVFVTAANVTKFSTWANDAMSAPNLGMTEFKVF
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(TYEMBLrel. 03, Created)
(TYEMBLrel. 03, Last sequence update)
(TYEMBLrel. 22, Last annotation update)
38.0 kDa protein (PPE family protein).
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Microbac_PPE.
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23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
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Last
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                                                                                                                                                                                                               LGLRSGLSAGLAHAASAGLGQANLVGDLSVPPSWASATPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14D05073BF68028A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŚEQUENCE FROM N.A.

ŚTRAIN-CDC 1551 / Oshkosh;

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter

Fleischmann R.D., Alland D., Eisen J.A., Carpenter

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Hatt

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva

Belchei W., Utterback T., Weidman J., Khouri H., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical SEQUENCE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MT3221; -.
TubercuList; Rv3136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=H37RV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison
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PF00823; PPE; 1.
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AE007137; AAK47561.1;
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172; Conserv
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                                                                                                                                                                                                                  IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGI
                                                                                                                                                                                     LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPT----QGTTPSSKLGGLWKTVSPHRSPI
                                                                                                                                                                                                                                                                              SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                  VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                            TAQAAAVSQATDPLSL--LIETVTQALQALTIPSFIPEDFTFLDAIFAGYATVGVTQDVE
                                                                                                                                                                                                                                                                                                                                               MDFALLPPEVNSARMYTGPGAGSLLAAAGGWDSLAAELATTAEAYGSVLSGLAALHWRGP
       MLGGLPVGQMGARAGGGLSGVL-RVPPRPYVMPHSPAAG
                                       GAASVGNTVLASVGRANSIGQLSVPPSWAAPSTRPVSALSPAGLTTLPGTDVAEHGMPG-
                                                                GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSL--TSAAERG-PGQ
                                                                                                  SFVAGTIGAESNLGLLNVGDENPAEVTPGDFGIGELVSA----TSPGGGVSA-SGAG---
                                                                                                                            SNMVSM--ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSL
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380 AA; 37979 MW;
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Pred.
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345B1EF9EC9AE4AA CRC64;
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No. 4.4e-30;
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M.L., Haft
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H., Gill J.,
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Matches 161
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O33310; TremBirel. 05,
O1-JAN-1998 (TremBirel. 20,
O1-MAR-2002 (TremBirel. 20,
O1-OCT-2002 (TremBirel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO08967; CAA15564.1; ALT_INIT.
EMBL; AE0007111; AAK47157.1; -._
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Gwinn M., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Besham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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TubercuList; Rv2768c; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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RV2768C OR MT2838 OR MTV002.33C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whole genome comparison of Mycobacterium tuberculosis clinical
                                      308
                                                                                                                                                                                        189
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   292
                                                                                                                                                                                                               122 IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL 181
                                                                                                                                                                                                                                                               129
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                                                                                                                                                                                                                                                                                                                                                                        2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                 LEQAAAVEEASDTAAANQ-----LMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSP--H
                                                                                                                                                                                                                                                                                   SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
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                                    ITFVQNAINGAVN----TTAWFVMATIPNAVFLGHAFAALNPATVTAAADAVPAAAAAAG
                                                                                                                                                                                    VATNVLGQNTPAIMATEAHYGEMWAQDALAMYGYAASSA-AAGRLNPLITPSQTANMAGL
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                                                                         RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGV---RAMSS 291
                                                                                                                AGQAAAVSHAAAASTVQQVGLGSLISNLPNAVMGFASPLTSAADAAGLGGIIQDIEELLG
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70608
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connorr, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature A;Molecule type: DNA A;Residues: 1-391 <COL> A;Residues: 1-391 <COL> A;Cross-references: GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07839.1; PID:e311073; A;Experimental source: strain H37Rv C;Genetics: A;Status: preliminary; nucleic acid sequence not shown; translation not Query Match 100.0%; Score 1949; DB 2; Best Local Similarity 100.0%; Pred. No. 3.3e-108; Matches 391; Conservative 0; Mismatches 0; 121 LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVPAMSSLGSSLGSSG LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLILPFEEAPEMTSAGG ALIGNMENTS 391 Indels Length 391; 0 Gaps 120 360 180 360 120 240 240 60 300 300 180 60 0 Holroyd, Gordon, genome

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C;Species: Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70568
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
C;Accession: C70568
R;Cole, S.T.; Brosch, R.; Parkhill, M.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70568
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Cross-references: GB:Z75555;
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Pred. No. 6.4e-91;
lB; Mismatches 34;
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A; Experimental C; Genetics: A; Gene: PPE
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C;Species: Mycobacterium tuberculosis

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: G70929

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

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A;Residues: 1-393 <COL>
A;Cross-references: GB:Z95390; GB:AL123456;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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                                                                                                      MDFGALPPEVNSVRMYAGPGSAPMVAAASAWNGLAAELSSAATGYETVITQLSSEGWLGP
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                                                                                                                                                                                                             Conservative
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81.5%; Pred.
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Pred. No. 4.3e-39;
5; Mismatches 129
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l.4e-86;
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: A70932

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go;
C;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holrx

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Anthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: A70932

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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                                                                      SSL-GSSLGS-SGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSA-
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AERGPGQMLGGLPVGQMGARAGGGL----
                                                                                                                                                          RSPISNMVSMANNHMSMTNSGVS-----MTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAM
                                                                                                                                                                                                       AAQSAVVAQAAGAAASSDITAQLSQLISLLPSTLQSLA--TTATATSASAG--WDTV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDFGALPPEINSGRMYAGPGSGPLLAAAAAWDALAAELYSAAASYGSTIEGLTVAPWMGP
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                                                                                                                      LQSITTILANLTGPYSIIGLGAIPGGWWLTFGQILGLAQNAPGVAALLGPKAAAGALSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Holroyd,
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RESULT B70931

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

probable PPE protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change C;Accession: B70931

#text_change 22-Oct-1999

Holroyd,

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A;Residues: 1-403 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699;
A;Experimental source: strain H37Rv
C;Genetics:
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H70931
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: H70931
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C;Species: Mycobacterium tuberculosis
C;Date: 17-U1-1998 #sequence_revision 17-U1-1998 #text_change 22-Oct-1999
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;Gene: PPE
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Best Local
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                                                                    LGSÄLGGTPMVAPPPÄVAAG----MPGMPFGTMGGQGFG----RAVPQYGFRPNFVAR
                                                                                                        AARAL---PLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPP----RPYVMPH
                                                                                                                                                                 QTAAQNGVRAMSSLGSSL-----GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTP
                                                                                                                                                                                                                    WLDKLWALLDPN-----
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                                                                                                                                                                                                                                                                                        AAQSAAIAHATGASAGAQQTTLSQLIAAIPSVLQGLSSSTAATFASGPSGLLGIVGSGSS
                                                                                                                                                                                                                                                                                                                        LEQAAAVEEASDTAAA-----NQLMNNVPQALQQLAQPTQGT----
                                                                                                                                                                                                                                                                                                                                                                TATNVLGQNAPATAATEAQYAEMWSQDAMAMYGYAGASAAAT-QLTPFTEPVQTTNASGL
                                                                                                                                                                                                                                                                                                                                                                                         IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLDFEEAPEMTSAGGL
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                                                                                                                                            LGEATSG-----GLGGALVAPLGSAGGLGGTVAAGLGNAATVGTLSVPPSWTAAAPLASP
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403
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; Pred. No. 1.3e-36;
60; Mismatches 123;
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1618

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120

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ppE-family protein [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #t C;Accession: H87056 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.I. R;Cole, S.T.; Eiglmeier, K.; Dathoy, S.; Feltwell, T. e.am, M.A.; Rutherford, K.M.
                                                                                                                                                           Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, P.
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: H87056
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-421 <STO>
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A;Accession: B70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-423 <COL>
                                                                                                                      A;Cross-references:
C;Genetics:
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A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                   A;Gene: ML1182
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Best Local S
Matches 182
Query Match
Best Local Similarity
Matches 174; Conserv
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               37.5%;
nilarity 41.1%;
Conservative 5
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                 55;
                                                                                                                                       NID:g13093150;
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Pred. No. 1.7e-36;
0; Mismatches 123
            Score 731; DB 2;
Pred. No. 3.4e-36;
5; Mismatches 160
                                                                                                                                                                                                                                                                                                                                                , J.; James, K.D.;
S.; Feltwell, T.;
                                                                                                                                                                                                                                                                                                                                                                                                            20-Apr-2001 #text_change 20-Apr-2001
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                                                                                                                                       PIDN: CAC31563.1; GSPDB: GN00147
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                 160;
                                                 Length 421;
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                                                                                                                                                                                                                                                                                                                                              Thomson, N.R.; Wheeler, Fraser, A.; Hamlin, N.;
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                                                                                                                                                                                                                                                                                    Skelton,
               34;
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08
                                                                                                                                                                                                                                                                                    J.;
               Gaps
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                                                                                                                                                                                                                                                                                    Squares, R.;
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70925
C;Accession: G70925
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
C;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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G70925
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A;Authors: Sgares, R.; Sulston, J.E., Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70925
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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Best Local S
Matches 182
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                                                                                                                                                                                                                                                                                                       Similarity 41.8
32; Conservative
                                                                                      IATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
                                                                                                                                     AAASMVAAVTPYVAWLSATAGQAEQAGMQARAAAAYELAFAMTVPPPVVVANRALLVAL
                                                                                                                                                               SAGLMVAAAS PYVANMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
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            LEQAAA-----VEEASDTAAANQLMNN------VP--QALQQ-LAQPTQGTTPSSKL---
                                                     VATNFFGQNTPATAATEAQYAEMWAQDAAAMYAYAGSAATAT-ELTPFTAAPVTTSPAAL
                                                                                                                                                                                                                       MDFGVLPPEINSGRMYAGPGSGPMMAAAAAWDSLAAELGLAAGGYRLAISELTGAYWAGP
                                                                                                                                                                                                                                                              VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAARALPLTSLTSAAERGPGQML-GGLPVGQM---GARAGGGLSGVLRVPPRPYVMPHSP
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41.8%;
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                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                     Score 705; DB 2; I
Pred. No. 1.1e-34;
7; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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332

358

418

272

239 214 179 180

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PIDN:CAA98377.1;

PID:e1301025;

not

Holroyd, Gordon,

S Ø

genome

72;

Gaps

14;

60

181 120

179

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
(;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70625
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-391 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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Best Local Similarity
Matches 166; Conserv
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                                                                                 AGLADSVTPAGLGASLGEATLVGRLSVPAAWSTAAPATTAGATALEGSGWTVAAEEA-GP
                                                                                                                                                                                                                                                                                      LEQAAAVEEASDTAAANQ-----LMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRS
                                                                                                                                                                                                                                                                                                                                                                   IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATTILPFEEAPEMTSAGGL
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          VTGMMP-GMASAAKGTGAYAGPRYGFKPTVMP
                                                                                                                             SSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQ 353
                                                                                                                                                                     TPFVANIINSAVNTAAWYVNAAIPTAIFLANALNSGAPVAIAEGAIEAAEG---AASAAA
                                                                                                                                                                                                        P--ISNMVSMANNHMS-MTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLG
                                                                                                                                                                                                                                                  AAQSAAVGSAAATAAVNQVSVADLISSLPNAVSGLASPVTSVLDSTGLSGIIADIDALLA
                                                                                                                                                                                                                                                                                                                                VATNVLGINTPAIMATEALYAEMWAQDALAMYGYAAASG-AAGMLQPLSPPSQTTNPGGL
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                                                MLGGLPVGQMGARAGGGLSGVLRVPPRPYVMP 385
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Pred. No. 1.6e-34;
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            386
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R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hk Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
                                                                                                                                                                                                        RESULT
C70931
                                                                                                                                        probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
(;Species: Mycobacterium tuberculosis
(;Species: Mycobacterium tuberculosis
(;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
(;Accession: F7056)
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70560
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Best Local Similarity 39.1
Matches 168; Conservative
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TVIAQPPAGG
                                                         YVMPHSPAAG
                                                                                                                                                                                                                                                                                                                                                                                                             MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA---AAQAVQT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLATNFLGQNTAAIAATBAQYAEMWAQDAAAMYGYAGAGAAAT-QLSPENPAAQTINPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSAASMVAAATPQVAWLRSTAGQAEQAGSQAVAAASAYEAAFFATVPPPEIAANRALLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLDFAQLPPEVNSALMYAGPGSGPMLAAAAAWEALAAELQTTASTYDALITGLADGPWQG
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                                                                                                                  WTATTPAASPAVLAASNGLGAAAAAAEGSTHAFGGMPL--MGSGAGRAFNNFAAPRYGFKP
                                                                                                                                                                        WAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVL--RVPPRP 381
                                                                                                                                                                                                                               YFGLAHDLPKWASEGAKAAGEAAKALPAAVPAIPSAGL-SGVAGAVGQAASVGGLKVPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LASQAASVGQAVSGAANAQALTDIPKAL-----
                                                                                                                                                                                                                                                                                                                                                 ALGLTGHTWSSDGSGLIVGGVLGDFVQGVTGSÅELDÅSVÅMDTFGKWVSPARLMVTQFKD
                                                         391
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39.1%; Pred. No. 1.7e-34;
tive 61; Mismatches 145;
                                                                                                                                                                                                                                                                                        -AAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FGLSGIFTNEPPWLTDLGK 226
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Whitehead, S.; Barrell, B.G. tuberculosis from the complete

genome

Holroyd,

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Connor, R.; Davies, R.; Divier, R.; Seeger, K.; Skeiton, S.; Square, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skeiton, S.; Square, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G. A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete display. Apacession: A70500; MUID:98295987; PMID:9634230
A; Accession: B70932
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-468 < COL>
A; Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17730.1; PID A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                      probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70932
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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B70932
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A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA A;Residues: 1-463 <COL>A;Cross-references: GB:AL022021; GB:AL123456; NID:g32504 A;Experimental source: strain H37Rv
C;Genetics:
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Best Local S
Matches 174
                                                                             Query Match
Best Local Similarity
Matches 164; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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   MDFGLQPPEITSGEMYLGPGAGPMLAAAVAWDGLAAELQSMAASYASIVEGMASESWLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSLTS--AAERGPGOML---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SALGAGLGLRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSSLGSSLG----SSGLGG---GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSMLGLGFAESKMVLPANDTVISTIFGMVQFQKFFNPVTPFNPDLIPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGLQAVPAAAISEGSLLSQMALASVAGGALGGAAARATGGFLGGGRV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATOGVAVAQAVGASAGN-ARSLVSEVLEFLA--TAGTNYNKTVASLMNAVTGVPYASSVY
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                                                                                               35.0%;
40.9%;
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                                                                         Score 682.5; DB 2;
Pred. No. 2.8e-33;
9; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 688.5; DB 2;
Pred. No. 1.2e-33;
8; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGLPVGQMGARAGGGLSGVLRV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID: g3250699; PIDN: CAA17723.1; PID: e12546
                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

(Species: Mycobacterium tuberculosis

(CSpecies: Mycobacterium tuberculosis

(CASPECIA)

(CASPEC
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A;Residues: 1-380 <COL>
A;Cross-references: GB:Z83867; GB:AL123456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AAESMAVTAAPYIGWLYTTAEKTQQTAIQARAAALAFEQAYAMTLPPPVVAANRIQLLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSL--TSAAERG-PGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDFALLPPEVNSARMYTGPGAGSILLAAAGGWDSLAAELATTAEAYGSVLSGLAALHWRGP
                                                                                                                                                                    SFVAGTIGAESNLGLLNVGDENPAEVTPGDFGIGELVSA----TSPGGGVSA-SGAG---
                                                                                                                                                                                                                                                                      SNMVSM--ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSL
                                                                                                                                                                                                                                                                                                                                                                                    TAQAAAVSQATDPLSL--LIETVTQALQALTIPSFIPEDFTFLDAIFAGYATVGVTQDVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPT---QGTTPSSKLGGLWKTVSPHRSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IATNFFGQNTAAIAATEAQYAEMWAQDAAAMYGYATASA-AAALLTPFSPPRQTTNPAGL
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Pred. No. 6.1e-33;
6; Mismatches 143
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: G70881

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Mycobacterium tuberculocia
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A;Residues: 1-394 <COL>
A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15564.1; PID:e117389
A;Experimental source: strain H37Rv
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                                                                                                          PVAAMPGM-AGISGAAKGAGAYAGPRYGFKPIVMP 389
                                                                                                                                                       PGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMP 385
                                                                                                                                                                                                               LAHTVTPVGVGGASLTASLGEASSVGGLSVPAGWSTAAPAMTSGTTALEGSGWAVPEEAG
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